

|                       |   |  |   |  |
|-----------------------|---|--|---|--|
| QY                    | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480   | Db                                     | 107 FLKGRFVILRLKSEGRCQQLLAKPKQKQNSPFRGKESQPFNNKQPEPDTYFVKVYPP 166 |  |
| Db                    | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466   | QY                                     | 181 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| QY                    | 481 SBRALSKPPTAVYPPDYSCEGDPVPGPDLIPTKYMNDNQIOLCSDHHSRQHOLBPPGTR 540 | Db                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| Db                    | 467 SBRALSKPPTAVYPPDYSCEGDPVPGPDLIPTKYMNDNQIOLCSDHHSRQHOLBPPGTR 526 | QY                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| QY                    | 541 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDKPDKPDK 600   | Db                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| Db                    | 527 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDKPDKPDK 586   | QY                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQKQKQKQ 360 |  |
| QY                    | 601 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGATGAT 660 | Db                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQKQKQKQ 346 |  |
| Db                    | 587 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGATGAT 646 | QY                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| QY                    | 661 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQTSQ 720  | Db                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| Db                    | 647 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQTSQ 706  | QY                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| QY                    | 721 PPAKSKLSSGCKADLGCSITDHLAVAPL 753                                | Db                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| Db                    | 707 PPAKSKLSSGCKADLGCSITDHLAVAPL 739                                | QY                                     | 481 SSSALSKPLAVYPPDYSCEGDPVPGDLSKTRALDNPOLCSHHSRQHOLBPPGTR 540    |  |
| RESULT 3              | QDNPMT  | PRELIMINARY, PRT: 739 AA.              | Db  | 467 SBRALSKPPTAVYPPDYSCEGDPVPGDLSKTRALDNPOLCSHHSRQHOLBPPGTR 526  |
| AC                    | QDNPMT/   | (TREMBREL, 22, Created)                | QY  | 541 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDKPDK 600   |
| DT                    | 01-OCT-2002   | (TREMBREL, 22, Last sequence update)   | Db  | 527 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDKPDK 586   |
| DT                    | 01-MAR-2003   | (TREMBREL, 26, Last annotation update) | QY  | 601 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGAT 660 |
| DB                    | Interleukin 17 receptor-like protein long form.                     | Db                                     | 587 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGAT 646  |  |
| GN                    | NAME=IL17RA;  | QY                                     | 661 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQ 720   |  |
| OS                    | Homo sapiens (Human).   | Db                                     | 647 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQ 706   |  |
| OC                    | Dukarrota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;   | QY                                     | 721 PPAKSKLSSGCKADLGCSITDHLAVAPL 753                              |  |
| OC                    | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.          | Db                                     | 707 PPAKSKLSSGCKADLGCSITDHLAVAPL 739                              |  |
| OX                    | [1]   | QY                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| RP                    | SEQUENCE FROM N.A.  | Db                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| RA                    | PubMed:12998313; DOI:10.1074/jbc.M306936200;                        | QY                                     | 481 SSSALSKPLAVYPPDYSCEGDPVPGDLSKTRALDNPOLCSHHSRQHOLBPPGTR 540    |  |
| RA                    | Xiang S., Zhao Q., Rong G., Huang Y., Chen P., Zhang S.,            | Db                                     | 467 SBRALSKPPTAVYPPDYSCEGDPVPGDLSKTRALDNPOLCSHHSRQHOLBPPGTR 526   |  |
| RA                    | Liu L., Chang Z., Liu L., Pu X.Y., Chang Z.J.,                      | QY                                     | 541 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDK 600       |  |
| RL                    | Submitted (MAR-2002) to the GenBank/DDBJ databases.                 | Db                                     | 527 QGRRNPFKSKGKRSIYVACNMDPQDSDPDKPDKPDKPDKPDKPDKPDKPDK 586       |  |
| DR                    | AP492208; AAM74077.1; -.  | QY                                     | 601 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGAT 660  |  |
| DR                    | Genew; HGNC:1761; ILMND.  | Db                                     | 587 VLNDDMKCGPESDPLCKVBAVATGATGATGATGATGATGATGATGATGATGATGAT 646  |  |
| DR                    | GO:0006020; C:membrane; IBA.  | QY                                     | 661 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQ 720   |  |
| DR                    | GO:0004888; P:transmembrane receptor activity; IBA.                 | Db                                     | 647 LHTVKGSPDMPSQDQGIGNSVPSHSLPMLGSLDQTSQTSQTSQTSQTSQTSQTSQ 706   |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 721 PPAKSKLSSGCKADLGCSITDHLAVAPL 753                              |  |
| KW                    | Receptor.   | Db                                     | 707 PPAKSKLSSGCKADLGCSITDHLAVAPL 739                              |  |
| SQ                    | SEQUENCE FROM N.A.  | QY                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| Query Match           | 97.5%; Score 3915; DB 2; Length 739;                                | Db                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| Best Local Similarity | 97.5%; Pred. No. 4.5e-290;  | QY                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| Matches               | 737; Conservative 1; Mismatches 1; Indels 14; Gaps 1;               | Db                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| QY                    | 1 MAPMPLCSVPTVWACLSQVAVAGSGSGARAGTCTTCAAGAARPRCCTVANGC 60           | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| Db                    | 1 MAPMPLCSVPTVWACLSQVAVAGSGSGARAGTCTTCAAGAARPRCCTVANGC 66           | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| QY                    | 61 ASNNSGLYNTPKDCTTYLPNGRHTADQNTISQVACDQVAVTLPGLQIR 120             | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQKQKQ 360   |  |
| Db                    | 47 ASNNSGLYNTPKDCTTYLPNGRHTADQNTISQVACDQVAVTLPGLQIR 106             | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQKQ 346     |  |
| QY                    | 121 FLKGRFVILRLKSEGRCQQLLAKPKQKQNSPFRGKESQPFNNKQPEPDTYFVKV 180      | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | GO:0004888; P:transmembrane receptor activity; IBA.                 | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQKQ 360     |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQ 346       |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQKQ 360       |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQ 346         |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQKQ 360         |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQ 346           |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQKQ 360           |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQ 346             |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQKQ 360             |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQ 346               |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQKQ 360               |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQ 346                 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQKQ 360                 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQ 346                   |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQKQ 360                   |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 287 LKPVSPMAGPAPRIVAITVPLVIVSPLTQVYKQKQKQ 346                     |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 361 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 420            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 347 LPRBLAPEPKVYPPSKSGKQHMDPQDPEQCKVALLWDPEALCRSCB 406            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 421 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 480 |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 407 WYQKINHSQOPTIVVCSKGKMYPPDKKQYKHKKGCGGSGKERLPLVAVSIAIBKQDQ 466 |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 481 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 240    |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 167 PPKKESNTTIPPRTRCDQIQLPDLACKPMPKPRNTISQGSDMQVSQDPAHPPNG 226    |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 241 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 300            |  |
| DR                    | InterPro; IPR00157; TIR.  | QY                                     | 227 FPPPLVYKJHSGPPKAKTCQBOTTSCLQWSPDYLHLDVNTTRKMYA 286            |  |
| DR                    | InterPro; IPR00157; TIR.  | Db                                     | 301 LKPVSPMAGPAPRIVAITVPLVIVSPLTQ                                 |  |